
W P E R E H
(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Dec 23 10:08:06 1999; Maspar time 2.05 Seconds
Tabular output not generated. 82.845 Million cell updates/sec

Title: >US-09-177-843-1
Description: (1-6) from US09177843.ppe
Perfect Score: 41
Sequence: 1 GRGDSP 6

Scoring table: PAM 150
Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 18.809; Variance 16.648; scale 1.130

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	41	100.0	1256	1	FINC_CHICK FIBRONECTIN (FN) (FRAG	1.07e+00
2	41	100.0	1328	1	FINC_PLEWA FIBRONECTIN (FN) (FRAG	1.07e+00
3	41	100.0	2265	1	FINC_BOVIN FIBRONECTIN (FN).	1.07e+00
4	41	100.0	2386	1	FINC_HUMAN FIBRONECTIN PRECURSOR	1.07e+00
5	41	100.0	2477	1	FINC_MOUSE FIBRONECTIN PRECURSOR	1.07e+00
6	41	100.0	2477	1	FINC_RAT FIBRONECTIN PRECURSOR	1.07e+00
7	41	100.0	2481	1	FINC_XENLA FIBRONECTIN PRECURSOR.	1.07e+00
8	39	95.1	370	1	HUPK_RHILY HYDROGENASE EXPRESSION.	3.87e+00
9	38	92.7	425	1	YIK3_YEAST HYPOTHETICAL 48.3 KD P	7.22e+00
10	38	92.7	463	1	Y863_SYNY3 HYPOTHETICAL 50.4 KD P	7.22e+00
11	38	92.7	490	1	CP08_HUMAN CYTOCHROME P450 2C8 (E	7.22e+00
12	38	92.7	583	1	PUR6_CRYNE PHOSPHORIBOSYLAMINOIM	7.22e+00
13	38	92.7	825	1	SE5_RAT SE5 ANTIGEN.	7.22e+00
14	38	92.7	1266	1	NGCA_CHICK NEURONAL-GLIAL CELL AD	7.22e+00
15	37	90.2	235	1	NHAB_RHOSO NITRILE HYDRATASE SUBU	1.33e+01
16	37	90.2	492	1	CP51_PIG CYTOCHROME P450 XXIA1	1.33e+01
17	37	90.2	492	1	CP53_PIG CYTOCHROME P450 XXIA3	1.33e+01
18	37	90.2	495	1	CP51_BOVIN CYTOCHROME P450 2E1 (E	1.33e+01
19	37	90.2	715	1	Y07J_MYCTU HYPOTHETICAL 78.2 KD P	1.33e+01
20	37	90.2	953	1	YNN7_YEAST HYPOTHETICAL 109.8 KD	1.33e+01
21	36	87.8	294	1	POL_SNSAV POL POLYPROTEIN [CONTA	2.42e+01
22	36	87.8	336	1	FILA_MOUSE FILAGGRIN (FRAGMENT).	2.42e+01
23	36	87.8	388	1	REFC_CAUCR RECF PROTEIN.	2.42e+01

24	36	87.8	780	1	PRTP_HSV1P PROCESSING AND TRANSP	2.42e+01
25	36	87.8	1065	1	VINC_CHICK VINCULIN.	2.42e+01
26	36	87.8	1065	1	VINC_HUMAN VINCULIN.	2.42e+01
27	36	87.8	1065	1	VINC_MOUSE VINCULIN.	2.42e+01
28	36	87.8	1240	1	DPOL_HSV21 DNA POLYMERASE (EC 2.7	2.42e+01
29	35	85.4	277	1	HXDB_NOTVI HOMEBOX PROTEIN HOX-D	4.33e+01
30	35	85.4	339	1	YE73_SCHPO PUTATIVE 38.2 KD PHOSP	4.33e+01
31	35	85.4	350	1	RS40_ARATH ARGININE/SERINE-RICH S	4.33e+01
32	35	85.4	356	1	RS41_ARATH ARGININE/SERINE-RICH S	4.33e+01
33	35	85.4	389	1	NDPP_MOUSE NPC DERIVED PROLINE RI	4.33e+01
34	35	85.4	616	1	LEU1_CORGL 2-ISOPROPYLMALATE SYNT	4.33e+01
35	35	85.4	655	1	H570_DAUCA HEAT SHOCK 70 KD PROTE	4.33e+01
36	35	85.4	657	1	MY16_MOUSE MYELOID DIFFERENTIATIO	4.33e+01
37	35	85.4	829	1	TOP1_XENLA DNA TOPOISOMERASE I (E	4.33e+01
38	35	85.4	831	1	PRIA_SYNY3 PRIMOSOMAL PROTEIN N'	4.33e+01
39	35	85.4	860	1	AREA_PENRO NITROGEN REGULATING PR	4.33e+01
40	35	85.4	905	1	ATA1_SYNY3 CATION-TRANSPORTING AT	4.33e+01
41	35	85.4	917	1	NTA2_ARATH NITRATE REDUCTASE 2 (E	4.33e+01
42	35	85.4	1019	1	LFC_FACTR LIMULUS CLOTTING FACTO	4.33e+01
43	35	85.4	1093	1	YKD5_CAEEL PUTATIVE SERINE/THREON	4.33e+01
44	35	85.4	1926	1	LPH_RABIT LACTASE-PHLORIDIN HYDR	4.33e+01
45	35	85.4	2411	1	MYSA_DROME MYOSIN HEAVY CHAIN, MU	4.33e+01

ALIGNMENTS

RESULT 1	FINC_CHICK	STANDARD;	PRT; 1256 AA.
AC	P11722; 090921;		
DT	01-OCT-1989 (REL. 12, CREATED)		
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)		
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)		
DE	FIBRONECTIN (FN) (FRAGMENTS).		
GN	FNI.		
OS	GALLUS GALLUS (CHICKEN).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;		
OC	NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.		
[1]			
RP	SEQUENCE OF 1-50 FROM N.A.		
RA	MEDLINE; 83117850.		
RA	HIRANO H., YAMADA Y., SULLIVAN M., DE CROMBRUGHE B., PASTAN I.,		
RA	YAMADA K.M.;		
RT	"Isolation of genomic DNA clones spanning the entire fibronectin		
RT	gene.";		
RL	PROC. NATL. ACAD. SCI. U.S.A. 80:46-50(1983).		
[2]			
RP	SEQUENCE OF 51-1256 FROM N.A.		
RC	STRAIN-WHITE LEIGHORN;		
RA	NORTON P.A.;		
RL	SUBMITTED (FEB-1995) TO EMBL/GENBANK/DBJ DATA BANKS.		
[3]			
RP	SEQUENCE OF 227-415 FROM N.A.		
RX	MEDLINE; 96183658.		
RA	GEHRIS A.L., BRANDLI D.W., LEWIS S.D., BENNETT V.D.;		
RT	"The exon encoding the fibronectin type III-9 repeat is		
RT	constitutively included in the mRNA from chick limb mesenchyme and		
RT	cartilage.";		
RL	BIOCHIM. BIOPHYS. ACTA 1311:5-12(1996).		
[4]			
RP	SEQUENCE OF 327-599 FROM N.A.		
RX	MEDLINE; 88050950.		
RA	KUBOMURA S., OBARA M., KARASAKI Y., TANIGUCHI H., GOTOH S.,		
RA	TSUDA T., HIGASHI K., OHSATO K., HIARNO H.;		
RT	"Genetic analysis of the cell binding domain region of the chicken		
RT	fibronectin gene.";		
RL	BIOCHIM. BIOPHYS. ACTA 910:171-181(1987).		
[5]			
RP	SEQUENCE OF 413-1256 FROM N.A.		
RX	MEDLINE; 88142820.		
RA	NORTON P.A., HYNES R.O.;		
RT	"Alternative splicing of chicken fibronectin in embryos and in normal		
RT	and transformed cells.";		
RL	MOL. CELL. BIOL. 7:4297-4307(1987).		

FT DISULFID 1324 1324 INTERCHAIN (WITH 1320 OF OTHER CHAIN) (BY
SIMILARITY).
FT SITE 461 463 CELL ATTACHMENT SITE.
FT CARBOHYD 89 89 POTENTIAL.
SQ SEQUENCE 1328 AA; 145037 MW; 1139F7B6 CRC32;

Query Match 100.0%; Score 41; DB 1; Length 1328;
Best local similarity 100.0%; Pred. No. 1.07e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 460 GRGDSP 465
|||||
QY 1 GRGDSP 6

RESULT 3
ID FINC BOVIN STANDARD; PRT; 2265 AA.
AC P07589;
DT 01-APR-1988 (REL. 07, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE FIBRONECTIN (FN).
GN FN1.
OS BOS TAURUS (BOVINE).
OC EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.
RN [1]
RX MEDLINE: 87054047.
RA SKORSTENGAARD K., JENSEN M.S., SAHL P., PETERSEN T.E., MAGNUSSEN S.;
RT "Complete primary structure of bovine plasma fibronectin.";
RL EUR. J. BIOCHEM. 161:441-453(1986).
RN [2]
RP PARTIAL SEQUENCE.
RX MEDLINE: 83117805.
RA PETERSEN T.E., THORGERSEN H.C., SKORSTENGAARD K., VIBE-PEDERSEN K.,
RA SAHL P., SOTIRUP-JENSEN L., MAGNUSSEN S.;
RT "Partial primary structure of bovine plasma fibronectin: three types
of internal homology.";
RL PROC. NATL. ACAD. SCI. U.S.A. 80:137-141(1983).
RN [3]
RP SEQUENCE OF 2170-2265 FROM N.A.
RX MEDLINE: 83221567.
RA KORNBLIHT A.R., VIBE-PEDERSEN K., BARALLE F.E.;
RT "Isolation and characterization of cDNA clones for human and bovine
fibronectins.";
RL PROC. NATL. ACAD. SCI. U.S.A. 80:3218-3222(1983).
CC -!- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
HEALING, AND MAINTENANCE OF CELL SHAPE.
CC -!- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
TO A LESSER EXTENT HOMODIMERS.
CC -!- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED
BY HEPATOCYTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC
FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS
DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.
CC -!- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING
STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN
OTHERS. THESE DIFFERENCES ARE DUE TO ALTERNATIVE SPLICING.
CC -!- SIMILARITY: CONTAINS 12 FIBRONECTIN TYPE I DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE II DOMAINS.
CC -!- SIMILARITY: CONTAINS 16 FIBRONECTIN TYPE III DOMAINS.

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CC

EMBL; X00800; E18191; ALT_SEQ.
PIR; A26452; FNBO.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 12.
DR PFAM; PF00039; fn1; 12.
DR PFAM; PF00040; fn2; 2.
DR PFAM; PF00041; fn3; 15.
DR HSSP; P02751; 2FN2.
KW GLYCOPROTEIN; PLASMA; HEPARIN-BINDING; ACUTE PHASE; PHOSPHORYLATION;
CELL ADHESION; REPEAT; ALTERNATIVE SPLICING.
FT MOD_RES 1 1
FT DOMAIN 21 241
FT DOMAIN 277 577
FT DNA_BIND 876 1141
FT DOMAIN 1236 1509
FT DOMAIN 1600 1870
FT DOMAIN 1991 2216
FT DOMAIN 19 59
FT DOMAIN 64 107
FT DOMAIN 108 151
FT DOMAIN 153 197
FT DOMAIN 198 242
FT DOMAIN 275 314
FT DOMAIN 314 373
FT DOMAIN 374 438
FT DOMAIN 437 480
FT DOMAIN 485 527
FT DOMAIN 528 571
FT DOMAIN 578 669
FT DOMAIN 688 778
FT DOMAIN 779 874
FT DOMAIN 875 964
FT DOMAIN 965 1054
FT DOMAIN 1055 1141
FT DOMAIN 1142 1234
FT DOMAIN 1235 1325
FT DOMAIN 1326 1415
FT DOMAIN 1416 1509
FT DOMAIN 1510 1599
FT DOMAIN 1600 1691
FT DOMAIN 1692 1780
FT DOMAIN 1781 1870
FT DOMAIN 1871 1990
FT DOMAIN >1870 <1982
FT DOMAIN 1982 2061
FT DOMAIN 2083 2127
FT DOMAIN 2128 2170
FT DOMAIN 2172 2215
FT SITE 1493 1495
FT DISULFID 21 47
FT DISULFID 45 56
FT DISULFID 66 94
FT DISULFID 92 104
FT DISULFID 110 138
FT DISULFID 136 148
FT DISULFID 155 184
FT DISULFID 182 194
FT DISULFID 200 229
FT DISULFID 227 239
FT DISULFID 277 304
FT DISULFID 302 311
FT DISULFID 329 355
FT DISULFID 343 370
FT DISULFID 389 415
FT DISULFID 403 430
FT DISULFID 439 467
FT DISULFID 465 477
FT DISULFID 487 514
FT DISULFID 512 524
FT DISULFID 530 558
FT DISULFID 556 568
FT DISULFID 2085 2114

CELL-ATTACHMENT.
HEPARIN-BINDING 2.
FIBRIN-BINDING 2.
FIBRONECTIN TYPE-I 1.
FIBRONECTIN TYPE-I 2.
FIBRONECTIN TYPE-I 3.
FIBRONECTIN TYPE-I 4.
FIBRONECTIN TYPE-I 5.
FIBRONECTIN TYPE-I 6.
FIBRONECTIN TYPE-II 1.
FIBRONECTIN TYPE-II 2.
FIBRONECTIN TYPE-I 7.
FIBRONECTIN TYPE-I 8.
FIBRONECTIN TYPE-I 9.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 7.
FIBRONECTIN TYPE-III 8.
FIBRONECTIN TYPE-III 9.
FIBRONECTIN TYPE-III 10.
FIBRONECTIN TYPE-III 11 (EXTRA DOMAIN).
FIBRONECTIN TYPE-III 12.
FIBRONECTIN TYPE-III 13.
CONNECTING STRAND 3 (CS-3) (V REGION).
FIBRONECTIN TYPE-III 15.
FIBRONECTIN TYPE-III 16.
FIBRONECTIN TYPE-I 10.
FIBRONECTIN TYPE-I 11.
FIBRONECTIN TYPE-I 12.
CELL ATTACHMENT SITE.

FT DISULFID 2112 2124
 FT DISULFID 2130 2137
 FT DISULFID 2155 2167
 FT DISULFID 2174 2200
 FT DISULFID 2198 2209
 FT DISULFID 2246 2246 INTERCHAIN (WITH 2250 OF OTHER CHAIN).
 FT DISULFID 2250 2250 INTERCHAIN (WITH 2246 OF OTHER CHAIN).
 FT CARBOHYD 399 399 GLUCOSAMINE.
 FT CARBOHYD 497 497 GLUCOSAMINE.
 FT CARBOHYD 511 511 GLUCOSAMINE.
 FT CARBOHYD 846 846 GLUCOSAMINE.
 FT CARBOHYD 976 976 GLUCOSAMINE.
 FT CARBOHYD 1213 1213 GLUCOSAMINE.
 FT CARBOHYD 1987 1987 GALACTOSAMINE.
 FT CARBOHYD 1943 1943 GALACTOSAMINE.
 FT CARBOHYD 1944 1944 GALACTOSAMINE.
 FT MOD_RES 2263 2263 PHOSPHORYLATION.
 SQ SEQUENCE 2265 AA; 249557 MW; B5176597 CRC32;

 Query Match 100.0%; Score 41; DB 1; Length 2265;
 Best Local Similarity 100.0%; Pred. No. 1.07e+00;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Db 1492 GRGDSP 1497
 QY 1 GRGDSP 6

 RESULT 4
 ID FINC HUMAN STANDARD; PRT; 2386 AA.
 AC P02751; Q14326;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE FIBRONECTIN PRECURSOR (FN).
 GN FN1 OR FN.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE OF 1-38 FROM N.A.
 RX MEDLINE; 87030890
 RA GUTMAN A., YAMADA K.M., KORNBLIHT A.;
 RT "Human fibronectin is synthesized as a pre-propolypeptide.";
 RL FEBS LETT. 207:145-148(1986).
 RN [2]
 RP SEQUENCE OF 1-49 FROM N.A.
 RX MEDLINE; 87175578
 RA DEAN D.C., BOWLUS C.L., BOURGEOIS S.;
 RT "Cloning and analysis of the promotor region of the human fibronectin gene.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 84:1876-1880(1987).
 RN [3]
 RP SEQUENCE OF 32-2081 AND 2113-2386 FROM N.A.
 RX MEDLINE; 85284965.
 RA KORNBLIHT A.R., UMEZAWA K., VIBE-PEDERSEN K., BARALLE F.E.;
 RT "Primary structure of human fibronectin: differential splicing may generate at least 10 polypeptides from a single gene.";
 RL EMBO J. 4:1755-1759(1985).
 RN [4]
 RP SEQUENCE OF 973-2081 AND 2113-2386 FROM N.A.
 RX MEDLINE; 84272258.
 RA KORNBLIHT A.R., VIBE-PEDERSEN K., BARALLE F.E.;
 RT "Human fibronectin: cell specific alternative mRNA splicing generates polypeptide chains differing in the number of internal repeats.";
 RL NUCLEIC ACIDS RES. 12:5853-5868(1984).
 RN [5]
 RP SEQUENCE OF 1594-2386 FROM N.A.
 RX MEDLINE; 85280409.
 RA BERNARD M.P., KOLBE M., WEIL D., CHU M.-L.;
 RT "Human cellular fibronectin: comparison of the carboxyl-terminal portion with rat identifies primary structural domains separated by hypervariable regions.";
 RL

RL BIOCHEMISTRY 24:2698-2704(1985).
 RN [6]
 RP SEQUENCE OF 32-290.
 RX MEDLINE; 84032463.
 RA GARCIA-PARDO A., PEARLSTEIN E., FRANGIONE B.;
 RT "Primary structure of human plasma fibronectin. The 29,000-dalton NH2-terminal domain.";
 RL J. BIOL. CHEM. 258:12670-12674(1983).
 RN [7]
 RP SEQUENCE OF 309-608, AND COLLAGEN-BINDING.
 RX MEDLINE; 87080265.
 RA OWENS R.J., BARALLE F.E.;
 RT "Mapping the collagen-binding site of human fibronectin by expression in Escherichia coli.";
 RL EMBO J. 5:2825-2830(1986).
 RN [8]
 RP SEQUENCE OF 1441-1548.
 RX MEDLINE; 82265604.
 RA PIERSCHBACHER M.D., RUOSLAHTI E., SUNDEIN J., LIND P., PETERSON P.A.;
 RT "The cell attachment domain of fibronectin. Determination of the primary structure.";
 RL J. BIOL. CHEM. 257:9593-9597(1982).
 RN [9]
 RP SEQUENCE OF 1434-1537 FROM N.A.
 RX MEDLINE; 83290929.
 RA OLDBERG A., LINNEY E., RUOSLAHTI E.;
 RT "Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell attachment domain in human fibronectin.";
 RL J. BIOL. CHEM. 258:10193-10196(1983).
 RN [10]
 RP SEQUENCE OF 1448-1540 FROM N.A.
 RX MEDLINE; 86111901.
 RA OLDBERG A., RUOSLAHTI E.;
 RT "Evolution of the fibronectin gene. Exon structure of cell attachment domain.";
 RL J. BIOL. CHEM. 261:2113-2116(1986).
 RN [11]
 RP SEQUENCE OF 1712-1739 FROM N.A.
 RX MEDLINE; 87026578.
 RA SEKIGUCHI K., KLOS A.M., KURACHI K., YOSHITAKE S., HAKOMORI S.;
 RT "Human liver fibronectin complementary DNAs: Identification of two different messenger RNAs possibly encoding the alpha and beta subunits of plasma fibronectin.";
 RL BIOCHEMISTRY 25:4936-4941(1986).
 RN [12]
 RP CHARACTERIZATION OF FIBRIN-BINDING SITE 1.
 RX MEDLINE; 95081153.
 RA ROSTAGNO A., WILLIAMS M.J., BARON M., CAMPBELL I.D., GOLD L.I.;
 RT "Further characterization of the NH2-terminal fibrin-binding site on fibronectin.";
 RL J. BIOL. CHEM. 269:31938-31945(1994).
 RN [13]
 RP STRUCTURE BY NMR OF 32-92.
 RX MEDLINE; 96069779.
 RA PORTS J.R., PHAN I., WILLIAMS M.J., CAMPBELL I.D.;
 RT "High-resolution structural studies of the factor XIIIa crosslinking site and the first type 1 module of fibronectin.";
 RL NAT. STRUCT. BIOL. 2:946-950(1995).
 RN [14]
 RP STRUCTURE BY NMR OF 182-275.
 RX MEDLINE; 94141923.
 RA WILLIAMS M.J., PHAN I., HARVEY T.S., ROSTAGNO A., GOLD L.I., CAMPBELL I.D.;
 RT "Solution structure of a pair of fibronectin type 1 modules with fibrin binding activity.";
 RL J. MOL. BIOL. 235:1302-1311(1994).
 RN [15]
 RP STRUCTURE BY NMR OF 406-464.
 RX MEDLINE; 98179558.
 RA STICHT H., PICKFORD A.R., PORTS J.R., CAMPBELL I.D.;
 RT "Solution structure of the glycosylated second type 2 module of fibronectin.";
 RL J. MOL. BIOL. 276:177-187(1998).

FN RP STRUCTURE BY NMR OF 1447-1540.
RX MEDLINE; 93046665.
RA MAIN A.L., HARVEY T.S., BARON M., BOYD J., CAMPBELL I.D.;
RT "The three-dimensional structure of the tenth type III module of
fibronectin: an insight into RGD-mediated interactions.";
RL CELL 71:671-678(1992).
RN [17]
RP STRUCTURE BY NMR OF 1447-1540.
RX MEDLINE; 92162710.
RA BARON M., MAIN A.L., DRISCOLL P.C., MARDON H.J., BOYD J.,
RA CAMPBELL I.D.;
RT "1H NMR assignment and secondary structure of the cell adhesion type
III module of fibronectin.";
RL BIOCHEMISTRY 31:2068-2073(1992).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 1447-1535.
RX MEDLINE; 94166075.
RA DICKINSON C.D., VEERAPANDIAN B., DAI X.-P., HAMLIN R.C., XUONG N.-H.,
RA RUOSLAHTI E., ELY K.R.;
RT "Crystal structure of the tenth type III cell adhesion module of
human fibronectin.";
RL J. MOL. BIOL. 236:1079-1092(1994).
RN [19]
RP FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
HEALING, AND MAINTENANCE OF CELL SHAPE.
CC [20]
RP SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
TO A LESSER EXTENT HOMODIMERS.
CC [21]
RP TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED
BY HEPATOCYTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC
FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS
DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.
CC [22]
RP ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING
STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN
OTHERS. THESE DIFFERENCES ARE DUE TO ALTERNATIVE SPLICING.
CC [23]
RP SIMILARITY: CONTAINS 12 FIBRONECTIN TYPE II DOMAINS.
CC [24]
RP SIMILARITY: CONTAINS 17 FIBRONECTIN TYPE III DOMAINS.
CC [25]
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CC [26]
EMBL; M15801; G553293; -
DR EMBL; X02761; G31397; -
DR EMBL; K00055; G182683; -
DR EMBL; M10905; G182697; -
DR EMBL; M12549; G553294; -
DR EMBL; M14059; G182703; -
DR PIR; A26460; FNHU.
DR PDB; ITTF; 31-JAN-94.
DR PDB; ITTG; 31-JAN-94.
DR PDB; IFNA; 30-APR-94.
DR PDB; IFNF; 29-JAN-96.
DR PDB; IFBR; 13-OCT-95.
DR PDB; 2FN2; PRELIMINARY.
DR MIM; 135600; -
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 12.
DR PFAM; PF00039; fn1; 12.
DR PFAM; PF00040; fn2; 2.
DR PFAM; PF00041; fn3; 16.
KW GLYCOPROTEIN; PLASMA; HEPARIN-BINDING; ACUTE PHASE; PHOSPHORYLATION;
KW SULFATATION; CELL ADHESION; REPEAT; ALTERNATIVE SPLICING; SIGNAL;
3D-STRUCTURE. 1 31

FT CHAIN 32 2386 FIBRONECTIN.
FT DOMAIN 52 272 FIBRIN- AND HEPARIN-BINDING 1.
FT DOMAIN 308 608 COLLAGEN-BINDING.
FT DNA_BIND 907 1172 CELL-ATTACHMENT.
FT DOMAIN 1267 1540 HEPARIN-BINDING 2.
FT DOMAIN 1721 1991 FIBRIN-BINDING 2.
FT DOMAIN 2206 2337 CELL ATTACHMENT SITE.
FT SITE 1524 1526 FIBRONECTIN TYPE-I 1.
FT DOMAIN 50 90 FIBRONECTIN TYPE-I 2.
FT DOMAIN 95 138
... Note: remainder of annotations omitted.
Query Match 100.0%; Score 41; DB 1; Length 2386;
Best Local Similarity 100.0%; Pred. NO. 1.07e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1523 GRGDSP 1528
Qy 1 GRGDSP 6
RESULT 5
ID FINC.MOUSE STANDARD; PRT: 2477 AA.
AC P11276; Q61568; Q61569; Q61567; Q64233;
DT 01-JUL-1989 (REL. 11, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE FIBRONECTIN PRECURSOR (FN) (FRAGMENTS).
GN FN1
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE OF 1-28 FROM N.A.
RC TISSUE=LIVER.
RX MEDLINE; 94131313.
RA POLLY P., NICHOLSON R.C.;
RT "Sequence of the mouse fibronectin-encoding gene promoter region.";
RL GENE 137:353-354(1993).
RN [2]
RP SEQUENCE OF 562-834 FROM N.A.
RC STRAIN=NMRL;
RX MEDLINE; 95403556.
RA TALTS J.F., WELLER A., TIMPL R., ERBLUM M., ERBLUM P.;
RT "Regulation of mesenchymal extracellular matrix protein synthesis by
transforming growth factor-beta and glucocorticoids in tumor
stroma.";
RL J. CELL SCI. 108:2153-2162(1995).
RN [3]
RP SEQUENCE OF 899-2376 FROM N.A.
RC GORSKI G., AROS M., NORTON P.;
RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [4]
RP SEQUENCE OF 2375-2477 FROM N.A.
RX MEDLINE; 88124987.
RA BLATTI S.P., FOSTER D.N., RANGANTHAN G., MOSES H.L., GETZ M.J.;
RT "Induction of fibronectin gene transcription and mRNA is a primary
response to growth-factor stimulation of AKR-2B cells.";
RL PROC. NATL. ACAD. SCI. U.S.A. 85:1119-1123(1988).
RN [5]
RP SEQUENCE OF 2375-2477 FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE; 93011702.
RA KHANDUAN E.W., SALOMON C., LEONARD N., TREMBLAY S., TURLER H.;
RT "Fibronectin gene expression in proliferating, quiescent, and SV40-
infected mouse kidney cells.";
RL EXP. CELL RES. 202:464-470(1992).
RN [6]
RP STRUCTURE BY NMR OF 1447-1630.
RX MEDLINE; 98202578.
RA COPIE V., TOMITA Y., AKIYAMA S.K., AOTA S., YAMADA K.M., VENABLE R.M.,
RA PASTOR R.W., KRUEGER S., TORCHIA D.A.;

"Solution structure and dynamics of linked cell attachment modules of mouse fibronectin containing the RGD and synergy regions: comparison with the human fibronectin crystal structure.";

J. MOL. BIOL. 277:663-682(1998).

1- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND HEALING, AND MAINTENANCE OF CELL SHAPE.

1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS; TO A LESSER EXTENT HOMODIMERS.

1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED BY HEPATOCYTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.

1- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN OTHERS. THESE DIFFERENCES ARE DUE TO ALTERNATIVE SPLICING.

1- SIMILARITY: CONTAINS 12 FIBRONECTIN TYPE I DOMAINS.

1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE II DOMAINS.

1- SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III DOMAINS.

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EMBL; 222729; G997912; -

DR EMBL; X82402; E122892; -

DR EMBL; X93167; E210659; -

DR EMBL; M18194; G387159; -

DR EMBL; S45680; G256716; -

DR PIR; A31371; A31371; -

DR PIR; C60597; C60597; -

DR PDB; 1MNF; 29-APR-98.

DR PDB; 2MNF; 29-APR-98.

DR MGI; 955566; FN1.

DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS00023; FIBRONECTIN_2; PARTIAL.

DR PROSITE; PS01253; FIBRONECTIN_1; 3.

DR PFAM; PF00039; fnl; 4.

DR PFAM; PF00041; fn3; 16.

KW GLYCOPROTEIN; PLASMA; HEPARIN-BINDING; ACUTE PHASE; PHOSPHORYLATION;

KW SULFATATION; CELL ADHESION; REPEAT; ALTERNATIVE SPLICING; SIGNAL;

3D-STRUCTURE. 1 32 BY SIMILARITY.

FT CHAIN 33 277 FIBRONECTIN.

FT DOMAIN 53 273 FIBRIN- AND HEPARIN-BINDING 1.

FT DNA_BIND 906 1171 COLLAGEN-BINDING.

FT DOMAIN 1357 1630 CELL-ATTACHMENT.

FT DOMAIN 1811 2081 HEPARIN-BINDING 2.

FT DOMAIN 2296 2427 FIBRIN-BINDING 2.

FT DOMAIN 51 96 FIBRONECTIN TYPE-I 1.

FT DOMAIN 96 140 FIBRONECTIN TYPE-I 2.

FT DOMAIN 140 185 FIBRONECTIN TYPE-I 3.

FT DOMAIN 185 230 FIBRONECTIN TYPE-I 4.

FT DOMAIN 230 272 FIBRONECTIN TYPE-I 5.

FT DOMAIN 306 343 FIBRONECTIN TYPE-I 6.

FT DOMAIN 345 404 FIBRONECTIN TYPE-II 1.

FT DOMAIN 405 469 FIBRONECTIN TYPE-II 2.

FT DOMAIN 468 516 FIBRONECTIN TYPE-I 7.

FT DOMAIN 516 559 FIBRONECTIN TYPE-I 8.

FT DOMAIN 559 602 FIBRONECTIN TYPE-I 9.

FT DOMAIN 609 706 FIBRONECTIN TYPE-III 1.

FT DOMAIN 707 808 FIBRONECTIN TYPE-III 2.

FT DOMAIN 809 903 FIBRONECTIN TYPE-III 3.

FT DOMAIN 904 994 FIBRONECTIN TYPE-III 4.

FT DOMAIN 995 1084 FIBRONECTIN TYPE-III 5.

FT DOMAIN 1085 1172 FIBRONECTIN TYPE-III 6.

FT DOMAIN	1173	1264	FIBRONECTIN TYPE-III 7.
FT DOMAIN	1265	1355	FIBRONECTIN TYPE-III 8 (EXTRA DOMAIN 1).
FT DOMAIN	1356	1446	FIBRONECTIN TYPE-III 9.
FT DOMAIN	1447	1536	FIBRONECTIN TYPE-III 10.
FT DOMAIN	1537	1630	FIBRONECTIN TYPE-III 11.
FT DOMAIN	1631	1720	FIBRONECTIN TYPE-III 12.
FT DOMAIN	1721	1810	FIBRONECTIN TYPE-III 13 (EXTRA DOMAIN 2).
FT DOMAIN	1811	1902	FIBRONECTIN TYPE-III 14.
FT DOMAIN	1903	1991	FIBRONECTIN TYPE-III 15.
FT DOMAIN	1992	2081	FIBRONECTIN TYPE-III 16.
FT DOMAIN	2082	2201	CONNECTING STRAND 3 (CS-3) (V REGION).
FT DOMAIN	>2081	<2202	FIBRONECTIN TYPE-III 17.
FT DOMAIN	2202	2283	FIBRONECTIN TYPE-III 18.
FT DOMAIN	2294	2338	FIBRONECTIN TYPE-I 10.
FT DOMAIN	2339	2381	FIBRONECTIN TYPE-I 11.
FT DOMAIN	2383	2426	FIBRONECTIN TYPE-I 12.
FT SITE	1614	1616	CELL ATTACHMENT SITE.
FT SITE	2181	2183	CELL ATTACHMENT SITE.
FT DISULFID	561	589	BY SIMILARITY.
FT DISULFID	587	599	BY SIMILARITY.
FT DISULFID	2296	2325	BY SIMILARITY.
FT DISULFID	2323	2335	BY SIMILARITY.
FT DISULFID	2341	2368	BY SIMILARITY.
FT DISULFID	2366	2378	BY SIMILARITY.
FT DISULFID	2385	2409	BY SIMILARITY.
FT DISULFID	2407	2423	BY SIMILARITY.
FT DISULFID	2458	2458	INTERCHAIN (WITH 2462 OF OTHER CHAIN).
FT DISULFID	2462	2462	INTERCHAIN (WITH 2458 OF OTHER CHAIN).
FT CARBOHYD	1006	1006	POTENTIAL.
FT CARBOHYD	1243	1243	POTENTIAL.
FT CARBOHYD	1290	1290	POTENTIAL.
FT CARBOHYD	2198	2198	POTENTIAL.
FT MOD_RES	2475	2475	PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT	2440	2440	N->T (IN REF. 5).
SEQ SEQUENCE	2477 AA; 271416 MW; 744ECC2B CRC32;		

Query Match 100.0%;

Best Local Similarity 100.0%; Score 41; DB 1; Length 2477;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1613 GRGDSP 1618

Qy 1 GRGDSP 6

RESULT 6	STANDARD;	PRT; 2477 AA.
ID FNC_RAT		
AC P04937;		
DT 13-AUG-1987 (REL. 05, CREATED)		
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)		
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)		
DE FIBRONECTIN PRECURSOR (FN).		
GN FNI.		
OS RATTUS NORVEGICUS (RAT).		
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;		
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.		
[1]		
RP SEQUENCE FROM N.A.		
RC STRAIN-FISHER; TISSUE-LIVER;		
RX MEDLINE; 88054951.		
RA SCHWARZBAUER J.E.; PATEL R.S.; FONDA D.; HYNES R.O.;		
RT "Multiple sites of alternative splicing of the rat fibronectin gene transcript.";		
RL EMBO J. 6:2573-2580(1987).		
[2]		
RP SEQUENCE OF 1-139 AND 2382-2477 FROM N.A.		
RC STRAIN-FISHER; TISSUE-LIVER;		
RX MEDLINE; 88054950.		
RA PATEL R.S.; ODERMATT E.; SCHWARZBAUER J.E.; HYNES R.O.;		
RT "Organization of the fibronectin gene provides evidence for exon shuffling during evolution.";		
RL EMBO J. 6:2565-2572(1987).		
[3]		

RP SEQUENCE OF 1586-2477 FROM N.A.
RX MEDLINE: 84082067.
RA SCHWARZBAUER J.E., TAMKUN J.W., LEMISCHKA I.R., HYNES R.O.;
RT "Three different fibronectin mRNAs arise by alternative splicing
RL CELL 35:421-431(1993).
CC -1- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
CC HEALING, AND MAINTENANCE OF CELL SHAPE.
CC -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
CC VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
CC TO A LESSER EXTENT HOMODIMERS.
CC -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED
CC BY HEPATOCYTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC
CC FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS
CC DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.
CC -1- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING
CC STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN
CC OTHERS. THESE DIFFERENCES ARE DUE TO ALTERNATIVE SPLICING.
CC -1- SIMILARITY: CONTAINS 12 FIBRONECTIN TYPE I DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE II DOMAINS.
CC -1- SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III DOMAINS.
CC -----
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CC -----
DR EMBL: X15906; G56164; -
DR EMBL: L29191; G204156; -
DR EMBL: L00191; G204156; JOINED.
DR EMBL: L29191; G204157; -
DR EMBL: L00191; G204157; JOINED.
DR EMBL: L29191; G204158; -
DR EMBL: L00191; G204158; JOINED.
DR EMBL: X05831; G56156; -
DR EMBL: X05832; G769820; -
DR EMBL: X05833; G773260; -
DR EMBL: X05834; G773261; -
DR PIR: A27252; A27252;
DR PIR: S00459; S00459;
DR PIR: S14428; S14428.
DR PROSITE: PS00022; EGF_1; 2.
DR PROSITE: PS00023; FIBRONECTIN_2; 2.
DR PROSITE: PS01253; FIBRONECTIN_1; 12.
DR PFAM: PF00039; fn1; 12.
DR PFAM: PF00040; fn2; 2.
DR PFAM: PF00041; fn3; 17.
DR HSP: P02751; 1FBR.
KW GLYCOPROTEIN; PLASMA; HEPARIN-BINDING; ACUTE PHASE; PHOSPHORYLATION;
KW SULFATATION; CELL ADHESION; REPEAT; ALTERNATIVE SPLICING; SIGNAL.
FT SIGNAL 1 32
FT CHAIN 33 2477 FIBRONECTIN.
FT DOMAIN 53 273 FIBRIN- AND HEPARIN-BINDING 1.
FT DOMAIN 308 608 COLLAGEN-BINDING.
FT DNA_BIND 906 1171
FT DOMAIN 1357 1630 CELL-ATTACHMENT.
FT DOMAIN 1811 2081 HEPARIN-BINDING 2.
FT DOMAIN 2296 2427 FIBRIN-BINDING 2.
FT DOMAIN 51 91 FIBRONECTIN TYPE-I 1.
FT DOMAIN 96 139 FIBRONECTIN TYPE-I 2.
FT DOMAIN 140 183 FIBRONECTIN TYPE-I 3.
FT DOMAIN 185 229 FIBRONECTIN TYPE-I 4.
FT DOMAIN 230 274 FIBRONECTIN TYPE-I 5.
FT DOMAIN 306 345 FIBRONECTIN TYPE-I 6.
FT DOMAIN 345 404 FIBRONECTIN TYPE-II 1.
FT DOMAIN 405 469 FIBRONECTIN TYPE-II 2.
FT DOMAIN 468 511 FIBRONECTIN TYPE-I 7.
FT DOMAIN 516 558 FIBRONECTIN TYPE-I 8.

FT DOMAIN 559 602 FIBRONECTIN TYPE-I 9.
FT DOMAIN 609 706 FIBRONECTIN TYPE-III 1.
FT DOMAIN 707 808 FIBRONECTIN TYPE-III 2.
FT DOMAIN 809 903 FIBRONECTIN TYPE-III 3.
FT DOMAIN 904 994 FIBRONECTIN TYPE-III 4.
FT DOMAIN 995 1084 FIBRONECTIN TYPE-III 5.
FT DOMAIN 1085 1172 FIBRONECTIN TYPE-III 6.
FT DOMAIN 1173 1264 FIBRONECTIN TYPE-III 7.
FT DOMAIN 1265 1355 FIBRONECTIN TYPE-III 8 (EXTRA DOMAIN 1).
FT DOMAIN 1356 1446 FIBRONECTIN TYPE-III 9.
FT DOMAIN 1447 1536 FIBRONECTIN TYPE-III 10.
FT DOMAIN 1537 1630 FIBRONECTIN TYPE-III 11.
FT DOMAIN 1631 1720 FIBRONECTIN TYPE-III 12.
FT DOMAIN 1721 1810 FIBRONECTIN TYPE-III 13 (EXTRA DOMAIN 2).
FT DOMAIN 1811 1902 FIBRONECTIN TYPE-III 14.
FT DOMAIN 1903 1991 FIBRONECTIN TYPE-III 15.
FT DOMAIN 1992 2081 FIBRONECTIN TYPE-III 16.
FT DOMAIN 2082 2201 CONNECTING STRAND 3 (CS-3) (V REGION).
FT DOMAIN >2081 2202 FIBRONECTIN TYPE-III 17.
FT DOMAIN 2202 2283 FIBRONECTIN TYPE-III 18.
FT DOMAIN 2283 2338 FIBRONECTIN TYPE-I 10.
FT DOMAIN 2338 2381 FIBRONECTIN TYPE-I 11.
FT DOMAIN 2383 2426 FIBRONECTIN TYPE-I 12.
FT SITE 1614 1616 CELL ATTACHMENT SITE.
FT SITE 2181 2183 CELL ATTACHMENT SITE.
FT DISULFID 53 79 BY SIMILARITY.
FT DISULFID 77 88 BY SIMILARITY.
FT DISULFID 98 126 BY SIMILARITY.
FT DISULFID 124 136 BY SIMILARITY.
FT DISULFID 142 170 BY SIMILARITY.
FT DISULFID 168 180 BY SIMILARITY.
FT DISULFID 187 216 BY SIMILARITY.
FT DISULFID 214 226 BY SIMILARITY.
FT DISULFID 232 261 BY SIMILARITY.
FT DISULFID 259 271 BY SIMILARITY.
FT DISULFID 308 335 BY SIMILARITY.
FT DISULFID 333 342 BY SIMILARITY.
FT DISULFID 360 386 BY SIMILARITY.
FT DISULFID 374 401 BY SIMILARITY.
FT DISULFID 420 446 BY SIMILARITY.
FT DISULFID 434 461 BY SIMILARITY.
FT DISULFID 470 498 BY SIMILARITY.
FT DISULFID 496 508 BY SIMILARITY.
FT DISULFID 518 545 BY SIMILARITY.
FT DISULFID 561 589 BY SIMILARITY.
FT DISULFID 587 599 BY SIMILARITY.
FT DISULFID 2296 2325 BY SIMILARITY.
FT DISULFID 2323 2335 BY SIMILARITY.
FT DISULFID 2341 2368 BY SIMILARITY.
FT DISULFID 2366 2378 BY SIMILARITY.
FT DISULFID 2385 2409 BY SIMILARITY.
FT DISULFID 2407 2423 BY SIMILARITY.
FT DISULFID 2458 2458 INTERCHAIN (WITH 2462 OF OTHER CHAIN).
FT DISULFID 2462 2462 INTERCHAIN (WITH 2458 OF OTHER CHAIN).
FT CARBOHYD 430 430 POTENTIAL.
FT CARBOHYD 528 528 POTENTIAL.
FT CARBOHYD 542 542 POTENTIAL.
FT CARBOHYD 876 876 POTENTIAL.
FT CARBOHYD 1006 1006 POTENTIAL.
FT CARBOHYD 1243 1243 POTENTIAL.
FT CARBOHYD 1290 1290 POTENTIAL.
FT CARBOHYD 2198 2198 POTENTIAL.
FT MOD_RES 2475 2475 PHOSPHORYLATION (BY SIMILARITY).
FT VARSPPLIC 1720 1809 MISSING (IN ALTERNATIVE SPLICED FORM).
FT VARSPPLIC 2082 2106 MISSING (IN CLONE LAMBDA-RLF4-5).
FT VARSPPLIC 2082 2200 MISSING (IN CLONE LAMBDA-RLF6).
FT CONFLICT 2318 2318 G -> A (IN REF. 3).
SQ SEQUENCE 2477 AA; 272510 MW; 093A8F76 CRC32;

Query Match 100.0%; Score 41; DB 1; Length 2477;
Best Local Similarity 100.0%; Pred. No. 1.07e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Db 1613 GRGDSF 1618
   |||||
QY 1 GRGDSF 6

RESULT 7
ID FNC_XENLA STANDARD; PRT: 2481 AA.
AC Q91740;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE FIBRONECTIN PRECURSOR.
GN FNI.
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
OC MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92111942.
RA DESIMONE D.W., NORTON P.A., HYNES R.O.;
RT "Identification and characterization of alternatively spliced
  fibronectin mRNAs expressed in early Xenopus embryos.";
RL DEV. BIOL. 149:357-369(1992).
CC -1- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
  INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
  ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
  HEALING, AND MAINTENANCE OF CELL SHAPE (BY SIMILARITY).
CC -1- SUBUNIT: DIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED VARIANTS,
  CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS (BY
  SIMILARITY).
CC -1- TISSUE SPECIFICITY: IN EARLY XENOPUS EMBRYO, CELLULAR FORMS OF
  FIBRONECTIN PREDOMINATE WHICH INCLUDE BOTH EXTRA DOMAINS. IN
  FIBRONECTIN OF EMBRYONIC AND ADULT LIVER THE CONNECTING STRAND 3
  CAN BE EITHER COMPLETELY EXCLUDED OR INCLUDED.
CC -1- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING
  STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN
  OTHERS. THESE DIFFERENCES ARE DUE TO ALTERNATIVE SPLICING.
CC -1- SIMILARITY: CONTAINS 12 FIBRONECTIN TYPE I DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE II DOMAINS.
CC -1- SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III DOMAINS.
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  or send an email to license@isb-sib.ch).
  -----
CC EMBL; M77820; G214134; -.
CC PROSITE; PS00022; EGF_1; 2.
CC PROSITE; PS01253; FIBRONECTIN_1; 11.
CC PFAM; PF00039; fnl; 12.
CC PFAM; PF00040; fn2; 2.
CC PFAM; PF00041; fn3; 17.
CC HSP; P02751; 2FN2.
CC GLYCOPROTEIN; PLASMA; HEPARIN-BINDING; ACUTE PHASE; CELL ADHESION;
  REPEAT; ALTERNATIVE SPLICING; SIGNAL.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 2481 FIBRONECTIN.
FT DOMAIN 55 275 FIBRIN- AND HEPARIN-BINDING 1.
FT DOMAIN 309 609 COLLAGEN-BINDING.
FT DNA_BIND 907 1172 BY SIMILARITY.
FT DOMAIN 1358 1631 CELL-ATTACHMENT.
FT DOMAIN 1812 2082 HEPARIN-BINDING 2.
FT DOMAIN 2301 2432 FIBRIN-BINDING 2.
FT DOMAIN 53 93 FIBRONECTIN TYPE-I 1.
FT DOMAIN 98 141 FIBRONECTIN TYPE-I 2.
FT DOMAIN 142 185 FIBRONECTIN TYPE-I 3.
FT DOMAIN 187 231 FIBRONECTIN TYPE-I 4.
FT DOMAIN 232 276 FIBRONECTIN TYPE-I 5.
FT DOMAIN 307 346 FIBRONECTIN TYPE-I 6.

DOMAIN 346 405 FIBRONECTIN TYPE-II 1.
DOMAIN 406 470 FIBRONECTIN TYPE-II 2.
DOMAIN 469 512 FIBRONECTIN TYPE-I 7.
DOMAIN 517 559 FIBRONECTIN TYPE-I 8.
DOMAIN 560 603 FIBRONECTIN TYPE-I 9.
DOMAIN 610 707 FIBRONECTIN TYPE-III 1.
DOMAIN 708 809 FIBRONECTIN TYPE-III 2.
DOMAIN 810 904 FIBRONECTIN TYPE-III 3.
DOMAIN 905 995 FIBRONECTIN TYPE-III 4.
DOMAIN 996 1085 FIBRONECTIN TYPE-III 5.
DOMAIN 1086 1173 FIBRONECTIN TYPE-III 6.
DOMAIN 1174 1265 FIBRONECTIN TYPE-III 7.
DOMAIN 1266 1356 FIBRONECTIN TYPE-III 8 (EXTRA DOMAIN).
DOMAIN 1357 1447 FIBRONECTIN TYPE-III 9.
DOMAIN 1448 1537 FIBRONECTIN TYPE-III 10.
DOMAIN 1538 1631 FIBRONECTIN TYPE-III 11.
DOMAIN 1632 1721 FIBRONECTIN TYPE-III 12.
DOMAIN 1722 1811 FIBRONECTIN TYPE-III 13 (EXTRA DOMAIN).
DOMAIN 1812 1903 FIBRONECTIN TYPE-III 14.
DOMAIN 1904 1992 FIBRONECTIN TYPE-III 15.
DOMAIN 1993 2082 FIBRONECTIN TYPE-III 16.
DOMAIN 2083 2205 CONNECTING STRAND 3 (CS-3) (V REGION).
DOMAIN >2082 FIBRONECTIN TYPE-III 17.
DOMAIN 2206 2287 FIBRONECTIN TYPE-III 18.
DOMAIN 2288 2343 FIBRONECTIN TYPE-I 10.
DOMAIN 2344 2386 FIBRONECTIN TYPE-I 11.
DOMAIN 2388 2431 FIBRONECTIN TYPE-I 12.
DOMAIN 1615 1617 CELL ATTACHMENT SITE.
DOMAIN 55 81 BY SIMILARITY.
DOMAIN 79 90 BY SIMILARITY.
DOMAIN 100 128 BY SIMILARITY.
DOMAIN 126 138 BY SIMILARITY.
DOMAIN 144 172 BY SIMILARITY.
DOMAIN 170 182 BY SIMILARITY.
DOMAIN 189 228 BY SIMILARITY.
DOMAIN 216 228 BY SIMILARITY.
DOMAIN 234 263 BY SIMILARITY.
DOMAIN 261 273 BY SIMILARITY.
DOMAIN 309 336 BY SIMILARITY.
DOMAIN 334 343 BY SIMILARITY.
DOMAIN 361 387 BY SIMILARITY.
DOMAIN 375 402 BY SIMILARITY.
DOMAIN 421 447 BY SIMILARITY.
DOMAIN 471 499 BY SIMILARITY.
DOMAIN 497 509 BY SIMILARITY.
DOMAIN 519 546 BY SIMILARITY.
DOMAIN 544 556 BY SIMILARITY.
DOMAIN 562 590 BY SIMILARITY.
DOMAIN 588 600 BY SIMILARITY.
DOMAIN 2301 2330 BY SIMILARITY.
DOMAIN 2328 2340 BY SIMILARITY.
DOMAIN 2345 2373 BY SIMILARITY.
DOMAIN 2371 2383 BY SIMILARITY.
DOMAIN 2390 2414 BY SIMILARITY.
DOMAIN 2412 2428 BY SIMILARITY.
DOMAIN 2459 2459 INTERCHAIN (WITH 2463 OF OTHER CHAIN) (BY
  SIMILARITY)
DOMAIN 2463 2463 INTERCHAIN (WITH 2459 OF OTHER CHAIN) (BY
  SIMILARITY).
DOMAIN 431 431 POTENTIAL.
DOMAIN 529 529 POTENTIAL.
DOMAIN 543 543 POTENTIAL.
DOMAIN 877 877 POTENTIAL.
DOMAIN 1244 1244 POTENTIAL.
DOMAIN 1291 1291 POTENTIAL.
DOMAIN 2202 2202 POTENTIAL.
SQ SEQUENCE 2481 AA; 272678 MW; 1C0F3341 CRC32;

Query Match 100.0%; Score 41; DB 1; Length 2481;
Best Local Similarity 100.0%; Pred. No. 1.07e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1614 GRGDSF 1619

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OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMETES; SACCHAROMYCETALES;

Query Match 92.7%; Score 38; DB 1; Length 463;
Best Local Similarity 66.7%; Pred. No. 7.22e+00;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 352 GRGETP 357
||||:|
Qy 1 GRGDSP 6

RESULT 11
ID CPC8_HUMAN STANDARD; PRT; 490 AA.
AC P10632;
DT 01-JUL-1989 (REL. 11, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE CYTOCHROME P450 2C8 (EC 1.14.14.1) (CYPLIC8) (P450 FORM 1) (P450 MP-
DE 12MP-20) (P450 1IC2) (S-MEPHENYTOIN 4-HYDROXYLASE).
GN CYP2C8.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA OKINO S.T., QUATTROCHI L.C., PENDURTHI U.R., MCBRIDE O.W.,
RA TUKEY R.H.;
RT "Characterization of multiple human cytochrome P-450 1 cDNAs. The
RT chromosomal localization of the gene and evidence for alternate RNA
RT splicing.";
RT J. BIOL. CHEM. 262:16072-16079(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88096500.
RA KIMURA S., PASTEWKA J., GELBOIN H.V., GONZALEZ F.J.;
RT "cDNA and amino acid sequences of two members of the human P450IIC
RT gene subfamily.";
RL NUCLEIC ACIDS RES. 15:10053-10054(1987).
RN [3]
RP SEQUENCE OF 11-490 FROM N.A.
RC TISSUE=LIVER;
RA GED C., UMBENHAUER D.R., BELLEW T.M., BORK R.W., SRIVASTAVA P.K.,
RA SHINRIKI N., LLOYD R.S., GUENGERICH F.P.;
RT "Characterization of cDNAs, mRNAs, and proteins related to human
RT liver microsomal cytochrome P-450 (S)-mephenytoin 4'-hydroxylase.";
RL BIOCHEMISTRY 27:6929-6940(1988).
RN [4]
RP SEQUENCE OF 281-490 FROM N.A.
RX MEDLINE; 91016847.
RA KOLYADA A.Y.;
RT "Sequence of a human liver cytochrome P-450 cDNA clone.";
RL NUCLEIC ACIDS RES. 18:5550-5550(1990).
CC -!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
CC ACIDS, AND XENOBIOTICS. IN THE EPOXYDATION OF ARACHIDONIC ACID
CC IT GENERATES ONLY 14,15- AND 11,12-CIS-EPOXYEICOSATRIENOIC ACIDS.
CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- INDUCTION: P450 CAN BE INDUCED TO HIGH LEVELS IN LIVER AND OTHER
CC TISSUES BY VARIOUS FOREIGN COMPOUNDS, INCLUDING DRUGS, PESTICIDES,
CC AND CARCINOGENS.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -!- CAUTION: ALTERNATIVE SPLICING HAS BEEN SHOWN TO OCCUR BUT THE
CC SHORTER FORMS ARE BELIEVED TO BE NON-FUNCTIONAL.

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CC EMBL; M17397; G181326; -
CC EMBL; M17398; G181328; ALT_SEQ.
CC EMBL; M21941; G181368; -
CC EMBL; M21942; G181370; ALT_INIT.
CC EMBL; X51535; G23885; -
CC EMBL; Y00496; G297404; -
CC PIR; A29782; A29782.
CC PIR; E28951; E28951.
CC PIR; S06306; S06306.
CC MIM; 601129; -
CC PROSITE; PS00086; CYTOCHROME_P450; 1.
CC PFAM; PF00067; P450; 1.
CC OXIDOREDUCTASE; MONOOXYGENASE; ELECTRON TRANSPORT; MEMBRANE; HEME;
KW MICROSOME; ENDOPLASMIC RETICULUM; POLYMORPHISM.
FT BINDING 435 HEME.
FT VARIAT 154 E -> D (IN MP-12).
FT VARIAT 193 N -> K (IN MP-20).
FT VARIAT 249 K -> R (IN MP-12).
FT VARIAT 411 H -> L (IN MP-20).
FT CONFLICT 130 T -> N (IN REF. 1).
FT CONFLICT 264 I -> M (IN REF. 1).
FT CONFLICT 399 K -> R (IN REF. 4).
SQ SEQUENCE 490 AA; 55824 MW; EE7C433E CRC32;

Query Match 92.7%; Score 38; DB 1; Length 490;
Best Local Similarity 83.3%; Pred. No. 7.22e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 96 GRGNP 101
||||:|
Qy 1 GRGDSP 6

RESULT 12
ID PUR6_CRYNE STANDARD; PRT; 583 AA.
AC Q92233;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE (EC 4.1.1.21) (AIR
DE CARBOXYLASE) (AIRC) (FRAGMENT).
GN ADE2.
OS CRYPTOCOCCUS NEOFORMANS (FILOBASIDIELLA NEOFORMANS).
OC EUKARYOTA; FUNGI; BASIDIOMYCOTA; HYMENOMYCETES; TREMBELLALES;
OC FILOBASIDIACEAE; FILOBASIDIELLA.
RN [1]
RP SEQUENCE FROM N.A.
RA PERFECT J.R.;
RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- CATALYTIC ACTIVITY: 1-(5-PHOSPHORIBOSYL)-5-AMINO-4-IMIDAZOLE-
CC CARBOXYLATE = 1-(5-PHOSPHORIBOSYL)-5-AMINOIMIDAZOLE + CO(2).
CC -!- PATHWAY: SIXTH STEP IN DE NOVO PURINE BIOSYNTHESIS.
CC -!- SIMILARITY: TO OTHER FUNGAL AND PLANT AIR CARBOXYLASE AND TO THE
CC AIR CARBOXYLASE PROTEINS, PURE AND PURK, FROM EUBACTERIA.
CC
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CC or send an email to license@isb-sib.ch).

CC EMBL; U70673; G1589929; -
CC PFAM; PF00731; AIRC; 1.
CC PURINE BIOSYNTHESIS; LYASE; DECARBOXYLASE.
FT NON_TER 1
SQ SEQUENCE 583 AA; 62557 MW; C3CF816F CRC32;

Query Match 92.7%; Score 38; DB 1; Length 583;
 Best Local Similarity 83.3%; Pred. No. 7.22e+00;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 162 GRGSP 167
 QY 1 GRGSP 6

RESULT 13
 ID SE5_RAT STANDARD; PRT; 825 AA.
 AC Q63003;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE SE5 ANTIGEN.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WISTAR; TISSUE-BRAIN;
 RX MEDLINE; 96015159.
 RA SUZUKI E., KOJIMA N., YOSHIMURA K., UYEMURA K., OBATA K., AKAGAWA K.;
 RT "Cloning and sequence analysis of cDNA for a possible DNA-binding
 protein SE5 in the nervous system.";
 RL J. BIOCHEM. 118:122-128(1995).
 CC -!- FUNCTION: MIGHT HAVE DNA-BINDING ABILITY.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN NEURONS.
 CC -----
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 CC -----
 CC EMBL; D37934; G531261; -
 DR DNA-BINDING; NUCLEAR PROTEIN; ANTIGEN.
 KW SEQUENCE 825 AA; 86831 MW; BC01D1EF CRC32;
 SQ

Query Match 92.7%; Score 38; DB 1; Length 825;
 Best Local Similarity 83.3%; Pred. No. 7.22e+00;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 430 GRGSP 435
 QY 1 GRGSP 6

RESULT 14
 ID NGCA-CHICK STANDARD; PRT; 1266 AA.
 AC Q03696;
 DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM).
 OS GALLUS GALLUS (CHICKEN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
 OC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE-BRAIN;
 RX MEDLINE; 91154306.
 RA BURGOON M.P., GRUMET M., MAURO V., EDELMAN G.M., CUNNINGHAM B.A.;
 RT "Structure of the chicken neuron-glia cell adhesion molecule, Ng-CAM:
 origin of the polypeptides and relation to the Ig superfamily.";
 RL J. CELL BIOL. 112:1017-1029(1991).
 RN [2]
 RP REVISIONS.

RA BURGOON M.P.;
 RL SUBMITTED (JUL-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -!- FUNCTION: MEDIATE THE ADHESION OF NEURONS TO NEURONS AND NEURONS
 CC TO GLIA. IT IS INVOLVED IN NEURONAL MIGRATION, NEURITE
 CC FASCICULATION AND OUTGROWTH. BINDS TO ITSELF AND TO AXONIN 1.
 CC -!- SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: BRAIN.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC 6 C2-LIKE DOMAINS.
 CC -!- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL; X56969; G509767; -
 DR PIR; A37967; A37967.
 DR PFAM; PF00041; fn3; 5.
 DR PFAM; PF00047; ig; 6.
 KW IMMUNOGLOBULIN FOLD; GLYCOPROTEIN; SIGNAL; CELL ADHESION; REPEAT;
 KW TRANSMEMBRANE.
 FT SIGNAL 1 20
 FT CHAIN 21 1266 NEURONAL-GLIAL CELL ADHESION MOLECULE.
 FT DOMAIN 21 1130 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1131 1153 POTENTIAL.
 FT DOMAIN 1154 1266 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 51 117 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 147 212 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 253 313 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 341 404 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 434 497 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 525 588 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 616 677 FIBRONECTIN TYPE-III.
 FT DOMAIN 716 784 FIBRONECTIN TYPE-III.
 FT DOMAIN 823 910 FIBRONECTIN TYPE-III.
 FT DOMAIN 945 1004 FIBRONECTIN TYPE-III.
 FT DOMAIN 1040 1098 FIBRONECTIN TYPE-III.
 FT SITE 914 916 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 58 110 POTENTIAL.
 FT DISULFID 154 205 POTENTIAL.
 FT DISULFID 260 306 POTENTIAL.
 FT DISULFID 348 397 POTENTIAL.
 FT DISULFID 441 490 POTENTIAL.
 FT DISULFID 532 581 POTENTIAL.
 FT CARBOHYD 97 97 POTENTIAL.
 FT CARBOHYD 288 288 POTENTIAL.
 FT CARBOHYD 390 390 POTENTIAL.
 FT CARBOHYD 434 434 POTENTIAL.
 FT CARBOHYD 472 472 POTENTIAL.
 FT CARBOHYD 498 498 POTENTIAL.
 FT CARBOHYD 712 712 POTENTIAL.
 FT CARBOHYD 819 819 POTENTIAL.
 FT CARBOHYD 1061 1061 POTENTIAL.
 FT CARBOHYD 1075 1075 POTENTIAL.
 FT CARBOHYD 1100 1100 POTENTIAL.
 FT CARBOHYD 1116 1116 POTENTIAL.
 SQ SEQUENCE 1266 AA; 136570 MW; 922E442E CRC32;

Query Match 92.7%; Score 38; DB 1; Length 1266;
 Best Local Similarity 83.3%; Pred. No. 7.22e+00;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 913 GRGSP 918
 QY 1 GRGSP 6

RESULT 15
 ID NHAB_RHOS STANDARD; PRT; 235 AA.

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AC Q53117;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE NITRILE HYDRATASE SUBUNIT BETA (EC 4.2.1.84) (NITRILASE) (NHASE).
GN NTHB.
OS RHODOCOCCLUS SP.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC ACTINOMYCETALES; CORYNEBACTERINEAE; NOCARDIACEAE; RHODOCOCCLUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92041549.
RA MAYAUX J.-F., CERBLAUD E., SOUBRIER F., YEH P., BLANCHE F., PETRE D.;
RT "Purification, cloning, and primary structure of a new enantiomer-
RT selective amidase from a Rhodococcus strain: structural evidence for
RT a conserved genetic coupling with nitrile hydratase.";
RL J. BACTERIOL. 173:6694-6704(1991).
CC -!- FUNCTION: NHASE CATALYZES THE HYDRATION OF VARIOUS NITRILE
CC COMPOUNDS TO THE CORRESPONDING AMIDES. INDUSTRIAL PRODUCTION OF
CC ACRYLAMIDE IS NOW BEING DEVELOPED USING SOME OF THESE ENZYMES.
CC -!- CATALYTIC ACTIVITY: AN ALIPHATIC AMIDE - A NITRILE + H(2)O.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SIMILARITY: TO OTHER NITRILE HYDRATASES SUBUNIT BETA.
CC -----
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CC -----
DR EMBL; M74531; G152053; -.
DR HSP; P13449; IAHJ.
KW LYASE.
SQ SEQUENCE 235 AA; 26078 MW; 355E3B38 CRC32;

Query Match 90.2%; Score 37; DB 1; Length 235;
Best Local Similarity 83.3%; Pred. NO. 1.33e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 185 GRGDDP 190
Qy 1 GRGDSP 6

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